

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2003, 12:29:01, Search time 2393 Seconds  
(without alignments)  
15773.026 Million cell updates/sec

Title: US-09-745-506-74  
Perfect score: 1553  
Sequence: 1 GTCATTGTCATCTGCGCT.....TCGTCTTACTTAACATTCAA 1553

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapept 1.0

Searched: 22781392 seqs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estln:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_man:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pio:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1034	66.6	1201 9	AL529615 AL529615
2	1014.2	65.3	1201 9	AL582089 AL582089
3	1008.4	64.9	1201 9	AL563496 AL563496
4	952.2	61.3	1117 12	BMS45164 BMS45164

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c	6	931.6	60.0	1201 9	AL581997
c	7	931.6	59.5	1201 13	BX446370
c	8	924.6	59.5	1201 13	BX377118
c	9	861	55.4	930 13	BX393871
c	10	860	55.4	1006 13	BX386928
c	11	855.6	55.1	984 13	BX385101
c	12	855.2	55.1	1376 11	AK011670
c	13	850.2	54.7	929 13	BUS95307
c	14	850	54.7	929 13	BQ927763
c	15	847.4	54.6	961 9	AL521919
c	16	841.4	54.1	857 13	BUI172435
c	17	839.8	54.2	1201 13	BUS23986
c	18	828.4	53.3	919 13	BUS26538
c	19	827.6	53.3	957 9	AL521920
c	20	823.6	53.0	1079 13	BX339175
c	21	818	52.7	997 13	BX386927
c	22	792.2	51.1	1467 11	AK003978
c	23	792.2	51.0	836 13	BQ229243
c	24	782.4	50.4	886 9	AL520537
c	25	770.6	49.6	890 9	AL520538
c	26	765.4	49.3	877 13	BQ437698
c	27	750.6	48.3	1019 12	BMS57530
c	28	750.4	48.3	888 13	BUI195469
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c	30	732.6	47.2	817 12	B1755123
c	31	731	47.1	742 12	B1093955
c	32	728.4	46.9	811 10	BG213848
c	33	725	46.7	796 9	AUI34237
c	34	723.2	46.6	963 10	BE797115
c	35	720.6	46.4	1919 11	AK076788
c	36	720.4	46.4	937 13	B0894563
c	37	712	45.8	871 12	BG765986
c	38	709.2	45.7	1119 10	BG745052
c	39	706	45.5	759 10	BE275324
c	40	705.4	45.4	1032 12	BM810545
c	41	704.8	45.4	732 10	BG472953
c	42	701.6	45.2	859 10	BE975933
c	43	698.4	45.0	909 14	CD385139
c	44	698	44.9	849 13	BUI19454
c	45	697.6	44.9	980 13	B0854847

## ALIGNMENTS

RESULT 1  
LOCUS AL529615 1201 bp mRNA linear EST 23-MAY-2003  
DEFINITION AL529615 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens  
CDNA clone CS0DD006YH18 5-PRIME, mRNA sequence.

ACCESSION AL529615  
VERSION AL529615.2 GI:31067458  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 1201)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
On Feb 13, 2001 this sequence version replaced g1.12793108.

Contact: Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

1287.f For more information about this cluster, see

http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DD006D090p1c1cluster=1287.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DD006DD090P1.

## FEATURES

source

1. 1201  
/organism="Homo sapiens"

/mol\_type="mRNA"  
/db\_xref="taxon:9606"

/clone="CS0DD006YH18"

/issue\_type="NEUROBLASTOMA COT 50-NORMALIZED"  
/clone.lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 319 a 286 c 274 g 299 t 23 others

ORIGIN

Query Match 66.6%; Score 1034; DB 9; Length 1201;  
Best Local Similarity 96.5%; Pred. No. 6.9e-269;  
Matches 1031; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

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187 AGTCCCAACAGACAGCCGGTTGTAGATTCCCTGATCTGCATTTCTCCGTTCCCTTCAAT 246
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173 GGAATTTGAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 232
307 TTGGGACATTTGGATTTCTGTTGAGAACCCACACACACACACACACACACACACACAC 366
233 TTGGGACATTTGGATTTCTGTTGAGAACCCACACACACACACACACACACACACACAC 292
367 CCTGACCAATGACTGACTGAGAAAGTGTGAGAGAGTGTCTGCAAAAGAGAGAGAGAGCT 426
293 CCTGACCAATGACTGACTGAGAAAGTGTGAGAGAGTGTCTGCAAAAGAGAGAGAGAGCT 352
427 CATTCTCTCTACCATCCGCTTATCTCTCCGACCATGAAGCGCATTAACCTTGAACACATG 486
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487 GAAGGAGCGCGTGGTGGATCCGGGCTCTGGAAGAACAGTGGTGGTGGTGGTGGTGGTGG 546
413 GAAGGAGCGCGTGGTGGATCCGGGCTCTGGAAGAACAGTGGTGGTGGTGGTGGTGGTGG 472
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473 AGCTATGATGCTGGCGCCAGAGGCGTCAACAAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 532
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533 TACCTCCAGGCCCATACATCTCTCCAAAGCTCCCAACTACCTACAGAGGGAAGACACCG 592
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593 ACTAATCAACGTTAATACACCCCAACACTGGCAAGTCTATCTCTGCAAGTGAAGG 652
727 AATTGACGCTGTTCTGCTACTTTCTTCTGCTAGAGTGGTAATGAGAAACAAACAG 786
653 AATTGACGCTGTTCTGCTACTTTCTTCTGCTAGAGTGGTAATGAGAAACAAACAG 712
787 GATTATCTGAATTTGACTCAGAGGCTTTGATGCAAGTGGTGGTGGTGGTGGTGGTGGTGG 846
713 GATTATCTGAATTTGACTCAGAGGCTTTGATGCAAGTGGTGGTGGTGGTGGTGGTGGTGG 772
847 CAACAACTTTATCAAGAAAGGAAATTTGTCACGAGGAGGAGGAGGAGGAGGAGGAGGAG 906
773 CAACAACTTTATCAAGAAAGGAAATTTGTCACGAGGAGGAGGAGGAGGAGGAGGAGGAG 832
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833 TGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 892

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QY 1027 AGAGTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1086
DB 953 AGAGTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1012
QY 1087 TGTGAGGCTGACCTTTTACCTCAGAGTGAAGTGTCCATCATGATATCTTTGGATGCTGC 1146
DB 1013 TGTGAGGCTGACCTTTTACCTCAGAGTGAAGTGTCCATCATGATATCTTTGGATGCTGC 1072
QY 1147 TTCCCAAGATTAATATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1206
DB 1073 TTCCCAAGATTAATATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1132
QY 1207 TGACCTTCGAGATATGCTGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1254
DB 1133 TGACCTTCGAGATATGCTGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1180

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## RESULT 2

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On Feb 16, 2001 this sequence version replaced gi:12949732.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 1287.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DL003BD12NP1&cluster=1287.f. Contact :  
Feng-Liang Email: fliang@liffech.com URL: <http://fulllength.invitrogen.com/InvitrogenCorporation1600FaradayAvenueGenoscopeSequenceID:CS0DL003BD12NP1>.

## FEATURES

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/organism="Homo sapiens"

/mol\_type="mRNA"  
/db\_xref="taxon:9606"

/clone="CS0DL003Y624"

/cell\_type="B CELLS (RAMOS CELL LINE)"  
/cell\_line="RAMOS CELL LINE"

/clone.lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 309 a 259 c 321 t 52 others

ORIGIN

Query Match 65.3%; Score 1014.2; DB 9; Length 1201;  
Best Local Similarity 92.6%; Pred. No. 1.6e-263;  
Matches 1063; Conservative 32; Mismatches 49; Indels 4; Gaps 4;

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 Db 1109 GGGGGGATGAAAAAGGAARCTTAATTTCTCTTACCATCCGCTTTCTCCAMCC 1050  
 QY 461 ATGAAGGCGATTAACCTGGACACATGAGAGGCGCTGTGATCCGGCTCTGGAGAAC 520  
 Db 1049 ATRAAGGCGATTAACCTGGACACATGAGAGGCGCTGTGATCCGGCTCTGGAGAAC 990  
 QY 521 AGATCGGATCTCTCTCTCATACAGCTATGATGCTGGCCCGGCGGTCAACAC 580  
 Db 989 AGATCGGATCTCTCTCTCATACAGCTATGATGCTGGCCCGGCGGTCAACAC 930  
 QY 581 TGGTGGCTAAAGGCTTGAGCTGTGCTCCAGGCGCCATACATCCCTTCAAGCTCC 640  
 Db 929 TKGTTGKCTAAAGGCTTGAGCTGTGCTCCAGGCGCCATACATCCCTTCAAGCTCC 871  
 QY 641 AACTACCTACAGAGGGAACACCGAGTAGAATTCACGTTAATACCCAGACCTG 700  
 Db 870 AACTACCTACAGAGGGAACACCGAGTAGAATTCACGTTAATACCCAGACCTG 811  
 QY 701 GACAAAGTCAATCTGCTGAGTGAAGAAATTAAGCTGTTCTGCTCTCTCTCTCT 760  
 Db 810 GACAAAGTCAATCTGCTGAGTGAAGAAATTAAGCTGTTCTGCTCTCTCTCTCT 751  
 QY 761 AGAGCTGGTAAAGGGAACAAACGATTAATGATGATGATGATGATGATGATG 820  
 Db 750 AGAGCTGGTAAAGGGAACAAACGATTAATGATGATGATGATGATGATGATG 691  
 QY 821 CAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 880  
 Db 690 CAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 631  
 QY 881 CTGAGAGAGCTTTGCTTCTCATACATGATGATGATGATGATGATGATGATG 940  
 Db 630 CTGAGAGAGCTTTGCTTCTCATACATGATGATGATGATGATGATGATGATG 571  
 QY 941 GTCCTCCGCGGACCATGATGATGATGATGATGATGATGATGATGATGATGATG 1000  
 Db 570 GTCCTCCGCGGACCATGATGATGATGATGATGATGATGATGATGATGATGATG 511  
 QY 1001 TTACCCCTTGGGCGGAGAGACCTTAGAGTCTCAAGTCAAGTCTGAGTCTGCT 1060  
 Db 510 TTACCCCTTGGGCGGAGAGACCTTAGAGTCTCAAGTCAAGTCTGAGTCTGCT 451  
 QY 1061 GGTCTCTGGAGACAGCTTCTGAGAGTCTGAGGCTGACCTTACCTCAGAGTGA 1120  
 Db 450 GGTCTCTGGAGACAGCTTCTGAGAGTCTGAGGCTGACCTTACCTCAGAGTGA 391  
 QY 1121 TCCCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1180  
 Db 390 TCCCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 331  
 QY 1181 AGCAAACTGAAAGAGCTTCTTCTGAGCTTGGAGATGATGATGATGATGATGAG 1240  
 Db 330 AGCAAACTGAAAGAGCTTCTTCTGAGCTTGGAGATGATGATGATGATGAG 271  
 QY 1241 AATTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATG 1300  
 Db 270 AATTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATG 211  
 QY 1301 CAGAAACATGAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1360  
 Db 210 CAGAAACATGAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 153  
 QY 1361 CATGAGTCAAGTGGAGCTGCTGCTTCCAGAGAGTGTCTTGAAGGATTAATTAAT 1420  
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QY 1481 ACCATATT 1488  
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 RESULT 3  
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 LOCUS  
 DEFINITION  
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 cDNA clone CS0DD006YH18 3-PRIME, mRNA sequence.  
 AL563496  
 VERSION  
 AL563496.2 GI:31287490  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 On Feb 15, 2001 this sequence version replaced gi:12912946.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 1287.f For more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgl-bln/cluster/cgl2seq-CS0DD006YH18NPLcluster-1287.f. Contact :  
 Feng Liang Email: fliang@life.com URL :  
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0DD006YH18NPL.  
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 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."  
 BASE COUNT  
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 325 a 268 c 278 g 298 t 32 others  
 Query Match 64.9%; Score 1008.4; DB 9; Length 1201;  
 Best Local Similarity 91.5%; Pred. No. 6e-262;  
 Matches 1102; Conservative 22; Mismatches 74; Indels 6; Gaps 6;  
 QY 325 ACTGTGGAGACCAACCCACACATGTAATACATGACCTCTGAGCAA-TGACCTGA 383  
 Db 1201 AMCTGTGTAACCAACCCACCACTGTAATAAATTTTCTCTACCAATATGCCCTRA 1142  
 QY 384 CTGAGGAAGTATGAGAGAGTGTGCAAAAGAGGACAGCTCAATCTCTCTACATC 443  
 Db 1141 CTGAGGAAGTATGAGAGAGTGTGCAAAAGAGGACAGCTCAATCTCTCTACATC 1083  
 QY 444 CGCCTATCTCCGA-CCCATGAAGGCAATACCTGGAACACATGGAAGAGGCGCTGG 502  
 Db 1082 CGCCTTCTTCCACCCCATTAAGGGGCAATACCTGGAACACATGGAAGAGGCGCTGG 1023  
 QY 503 ATCCGGGCTGAGAGACAGAGTGGTATCTACTCTCCATACAGACCTATGATCTGG 562  
 Db 1022 ATCCGGGCTGAGAGACAGAGTGGTATCTACTCTCCATACAGACCTTGTATSTGG 963  
 QY 563 CCCAGGGCGTCAACACTGTTGGCTAAAGGCTTGAAGCTTGAACCTCCAGG-CCCAT 621  
 Db 962 CCCAGGGCGTCAACACTGTTGGCTAAAGGCTTGAAGCTTGAACCTCCAGGCGCCAT 903

OY		622	ACATCTTCCAAAGCTTCACCACTACCCACGAGAGGAACAACCGAGTAGAATTCAAGCT	681
Dd		902	ACATCTTCCAAAGCTTCACCACTACCCACGAGAGGAACAACCGAGTAGAATTCAAGCT	843
OY		682	TAACTACACCAGAAGCTGGACAAGATCATGTCTGCAGTGAAAGGAATTGACGGTGTTC	741
Dd		842	TMACTACACCAGAAGCTGGACARAGTCATKTTCTCAGTAGAAGGAATTGACGGTGTTC	783
OY		742	TGTCACTCTTTTTCTGCTAGAGACTGGTAATGAGGAACAACACAGGATTTAATCTGAATTG	801
Dd		782	TGTCACTCTTTTTAAAAAATAAGAACCTGGTAATGAGGAACAACACAGGATTTAATCTGAATTG	723
OY		802	TACTCAGAAGGCTTTGATGACAGTGGTGGATTTTTCTCCGGAACAACAATTTATCA	861
Dd		722	TACTCAGAAGGCTTTGATGACAGTGGTGGATTTTTCTCCGGAACAACAATTTATCA	663
OY		862	GAAAGCGAAAATTTCTGTCACTGGAGAAACCTTTGCTTCTACATCTGGAATGGACGGTT	921
Dd		662	GAAAGCGAAAATTTCTGTCACTGGAGAAACCTTTGCTTCTACATCTGGAATGGACGGTT	603
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Dd		602	ATGCACACTGGATGAATCTGTCTCCCTGGCAACATGATTGATGAATPAAAAAGACACT	543
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Dd		542	AACACTCTCTATATTCGCTTAAGCCCTGGGGTGGGGAAGACCTTAGAGTCTCAAGTCAA	483
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Dd		362	TGTCACTCCTGTGTGAACACAGCAACACTGAAGAGAGCTTTCTTGTGACCTTCAGATAT	303
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Dd		302	GCTGGATTTCTCACTTGGAGAAATAGATTAATTTATCTATACAGAGCTGACAGGACCC	243
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OY		1402	GAGGGTATCATCATTTCCGGTTTGTTAATCTTATTCACCAAAATGTTCTANTGCTGTGAAG	1461
Dd		124	GAGGGTATCATCATTTCCGGTTTGTTAATCTTATTCACCAAAATGTTCTANTGCTGTGAAG	65
OY		1462	GTAACAACTGTATATATATACCATTTTAAATPAACAAATGTTCATATATTAACCTTAGAAA	1521
Dd		64	GTGAGASGTATATNTGACTACCATTTANATNAMAATAATGTTCAATTAATAATCTAGAGWD	5
OY		1522	GATT 1525	
Dd		4	GATT 1	
RESULT 4				
BMS45164				
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DEFINITION	AGENSCOURT_6497454 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5588986			
ACCESSION	BMS45164			
VERSION	BMS45164.1	GI:18777026		

KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 1117)
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished Contact: Robert Strusberg, Ph.D. Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a> Tissue Procurement: Invitrogen cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ULNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: L1AM12360 Row: P Column: 05 High quality sequence stop: 734. Location/Qualifiers
FEATURES	1..1117
SOURCE	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5588980" /lab_host="DH10B" /clone.lib="NIH MGC 125" /note="Organ: ovary (pool of 3); Vector: pCMV-Sport6; Site.1: EcoRV (destroyed); Site.2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
BASE COUNT	278 a 282 c 260 g 293 t 4 others
ORIGIN	
Query Match	61.3%; Score 952.2; DB 12; Length 1117;
Best Local Similarity	95.9%; Pred. No. 1e-246;
Matches 1050; Conservative	0; Mismatches 37; Indels 8; Gaps 7
QY	177 GGCATAGATGAGTCCCCACGACGACGCGGTGTGTGATTTCCCTGATCTGCATTTCTTCCC 236
DB	20 GGGATGGAGCTGTCCCCACGACGACGCGGTGTGTGATTTCCCTGATCTGCATTTCTTCCC 79
QY	237 GTTCCCTCATGATTTGAAGCTCTCCCTTCTCTCTTGAATGACTTTGCATCTCTCTGT 296
DB	80 GTTCCCTCATGATTTGAAGCTCTCTCTTCTCTCTTGAATGACTTTGCATCTCTCTGT 139
QY	297 TTGCTGAGAGTTGGACAAATGTTGATTACTGTGTGGAACCAAGCCACCACTACTGTAA 356
DB	140 TTGCTGAGAGTTGGACAAATGTTGATTACTGTGTGGAACCAAGCCACCACTACTGTAA 199
QY	357 ATACACCTTCTGACCAATGACCTGACGATGAGGAAGTATGAGGAAGAGGTGGCAAAAGA 416
DB	200 ATACACCTTCTGACCAATGACCTGACGATGAGGAAGTATGAGGAAGAGGTGGCAAAAGA 259
QY	417 AGCAGACCTATTTCTCTTACCAATTCGCGCTATTTCCGACCCATGGAAGCGCATAACT 476
DB	260 AGCAGACCTATTTCTCTTACCAATTCGCGCTATTTCCGACCCATGGAAGCGCATAACT 319
QY	477 GGAACACATGAGAGAGCGCCTGTGATCCGGGCTCTGAGAACAGAGTGGTATCTACT 536
DB	320 GGAACACATGAGAGAGCGCCTGTGATCCGGGCTCTGAGAACAGAGTGGTATCTACT 379
QY	537 CTCCTCATACAGCCATGATGTTGGGCCCAAGGGGCTCAACAAAGGTTGGCTAAAGGCG 596
DB	380 CTCCTCATACAGCCATGATGTTGGGCCCAAGGGGCTCAACAAAGGTTGGCTAAAGGCG 439
QY	597 TTGGAGCTTTGACTCCAGGCCCATATCTCTTCCAAAGCTTCCCAACTACCTACAGAG 656

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 Db 440 TTGGAGCTTACTACCTCCAGGCCATCATCTCTCCAAAGCTCCCACTACCTACAGAGG 499  
 Qy 657 GAAACCCGAGTGAATTTCAAGCTTAACTACACCCAAAGCTTGACAAAGCTATGCTG 716  
 Db 500 GAAACCCGAGTGAATTTCAAGCTTAACTACACCCAAAGCTTGACAAAGCTATGCTG 559  
 Qy 717 CAGTGAAGGAATTTGAGGCTTTCTGTCACTCTTTTCTGTGAGGAGCTGTGAATGAG 776  
 Db 560 CAGTGAAGGAATTTGAGGCTTTCTGTCACTCTTTTCTGTGAGGAGCTGTGAATGAG 619  
 Qy 777 AACAAACAGGATTAATCTGAATTTGACTAGAAAGCTTTGATGACAGGCTGTAGATTTTC 836  
 Db 620 AACAAACAGGATTAATCTGAATTTGACTAGAAAGCTTTGATGACAGGCTGTAGATTTTC 679  
 Qy 837 TTTCCCGGAAACAACTTTATCAGAAAGGAAATTTGCTACTGTGACGAAAGCTTTTTC 896  
 Db 680 TTTCCCGGAAACAACTTTATCAGAAAGGAAATTTGCTACTGTGACGAAAGCTTTTTC 739  
 Qy 897 TTTACATACATGGAATGGAAGGCTTATGACACATGGAATCTGTCTCCCTGGCAACCA 956  
 Db 740 TTTACATACATGGAATGGAAGGCTTATGACACATGGAATCTGTCTCCCTGGCAACCA 799  
 Qy 957 TGAATGATCGAATTAATAAGACACCTAAACTATCTCATTTGCTAGCCC-TTGGGGTG 1015  
 Db 800 TGAATGATCGAATTAATAAGACACCTAAACTATCTCATTTGCTAGCCC-TTGGGGTG 859  
 Qy 1016 GGGAGAACCTTAGAGTCTCAAGTCAAGTCTGG-CCCTGTGTCTGGTCTGGAGCAG 1074  
 Db 860 GGGAGAACCTTAGAGTCTCAAGTCAAGTCTGG-CCCTGTGTCTGGTCTGGAGCAG 919  
 Qy 1075 CGTTCACAGGCTTGAAGCTGACCTTACCTCAAGGAGTGAATGCTGCTCATGATAC 1134  
 Db 920 GTTCTCAAGGCTTGAAGCTGACCTTACCTCAAGGAGTGAATGCTGCTCATGATAC 979  
 Qy 1135 -TTTGGATGCTGCTTCCCAAGGAATTAAT-GTCATCTCTGTGAACACAGCAACACT-GA 1191  
 Db 980 TTTTGGATGCTGCTTCCCAAGGAATTAATGCTGCTGCTGTGAACACAGCAACACTGGA 1039  
 Qy 1192 ACAGAGCTTCTTTCTGACCTT-CGAGATATGCTGATTC--TCACCTTGCAATTAAGAT 1248  
 Db 1040 ACAGAGCTTCTTTCTGACCTTCCNAAGAAATGCTGAATCTCCCTGGGGGATTTAGA 1099  
 Qy 1249 AATATATATCTATC 1263  
 Db 1100 AATTTTTCCTATC 1114

RESULT 5  
 AL523985/c 1201 bp mRNA linear EST 22-MAY-2003  
 LOCUS AL523985 Homo sapiens NEUROBLASTOMA COR 25-NORMALIZED Homo sapiens  
 DEFINITION cDNA clone CS0DC003YB10 3-PRIME, mRNA sequence.  
 ACCESSION AL523985  
 VERSION AL523985.2 GI:31042246  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 1201)  
 L1.W.B., Gruber,C., Jessee,J. and Polayes,D.  
 Full-length cDNA libraries and normalization  
 Unpublished  
 On Feb 13, 2001 this sequence version replaced gi:12787478.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by life technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 1287.f for  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/

cg1-bin/cluster.cg1seq-CS0DC003DA05NP1cluster-1287.f. Contact :  
 Feng Liang Email : fliang@life.techn.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0DC003DA05NP1.

FEATURES  
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 1. 1201  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 323 a 249 c 273 g 320 t 36 others

ORIGIN

Query Match 60.1%; Score 933.2; Db 9; Length 1201;  
 Best Local Similarity 93.5%; Pred. No. 1.5e-241;  
 Matches 1029; Conservative 18; Mismatches 42; Indels 11; Gaps 7;

Qy 416 AAGCAGACCTATCTCTCTCCATCCGCTATCTCCGACCCATGAGCGCATACC 475  
 Db 1101 AAGAGCAGSCTATCTCTCTACCATCCCTTTCTCCACCATTAAGCGC--ATACC 1045  
 Qy 476 TGAACACATGGAAGAGACGCGCTGTGATCCGGGCTGTGAAGAACAGTGTGTATAC 535  
 Db 1044 TGKMACATATGG-AGGACGCGCTGTGATCCGGSTCT--GAGAACGAKY-C-GTWTCCAC 990  
 Qy 536 TCTCTCATAGGCTATGATGCTGCGGCCGACAGGCGTCAACAACTGGTGGCTAAAGG 595  
 Db 989 TCTCTCATAGGCTATGATGCTGCGGCCGACAGGCGTCAACAACTGGTGGCTAAAGG 930  
 Qy 596 CTGGAGCTTACTCTCCAGGCCCATATCATCTTCCAAAGCTCCCACTACCTACAGAG 655  
 Db 929 CTGGAGCTTACTCTCCAGGCCCATATCATCTTCCCAAGCTCCCACTACCTACAGAG 870  
 Qy 656 GGAACCCAGGATTAATCTGAATTTGACTAGAAAGCTTGAACAGCTGGAACAAAGCTATGCT 715  
 Db 869 GGAACCCAGGATTAATCTGAATTTGACTAGAAAGCTTGAACAGCTGGAACAAAGCTATGCT 810  
 Qy 716 GCAAGTGAAGGAATTTGAGGCTGCTGTCTGACTCTTTTCTGCTAGAGCTGTATAGAG 775  
 Db 809 GCAAGTGAAGGAATTTGAGGCTGCTGTCTGACTCTTTTCTGCTAGAGCTGTATAGAG 750  
 Qy 776 GAAACAAACGAGATTAATCTGAATTTGACTAGAAAGCTTGAACAGCTGGAACAAAGCTATGCT 835  
 Db 749 GAAACAAACGAGATTAATCTGAATTTGACTAGAAAGCTTGAACAGCTGGAACAAAGCTATGCT 690  
 Qy 836 CTTCCTCCGGAACAAACCTTTATCAGAAAGCGGAAATTTGCTGCTGAGAGAGCTTTG 895  
 Db 689 CTTCCTCCGGAACAAACCTTTATCAGAAAGCGGAAATTTGCTGCTGAGAGAGCTTTG 630  
 Qy 896 CTTCACATACATGGAATGGAAGGCTTATGCAACACTGATGATCTGTCTCCCTGGCAAC 955  
 Db 629 CTTCACATACATGGAATGGAAGGCTTATGCAACACTGATGATCTGTCTCCCTGGCAAC 570  
 Qy 956 ATGATTTGATCGAATTAATAAGACACCTTAATCTCATATTTGCTTACGCTTGGGGTG 1015  
 Db 569 ATGATTTGATCGAATTAATAAGACACCTTAATCTCATATTTGCTTACGCTTGGGGTG 510  
 Qy 1016 GGGAGAACCTTAGAGTCTCAAGTCAAGTCTGGGCGCTGTGCTGGGGAGCAGC 1075  
 Db 509 GGGAGAACCTTAGAGTCTCAAGTCAAGTCTGGGCGCTGTGCTGGGGAGCAGC 450  
 Qy 1076 GTTCTGAGAGGCTTGAAGCTGACCTTACTACAGAGTGAATGCTCCATCATGATACT 1135  
 Db 449 GTTCTGAGAGGCTTGAAGCTGACCTTACTACAGAGTGAATGCTCCATCATGATATTT 390  
 Qy 1136 TTTGATGCTCTTCCCAAGGAATTAATGCTATCTGTGTGAACACAGCAACCTGACGA 1195

Db	389	TTGATGTCGTCTCCCAAGGAATTAAGTATCTCTGTGTGAACACAGCAACACTGGAACA	330
QY	1196	GGCTTTCTTTTGACCTTCGAGATATGCTGGATTCTCACTTGAGGAATAGATAAATATT	1255
Db	329	GGCTTTCTTTTGACCTTCGAGGAATATGCTGATTTCTACTTGGAGGAATTAAGTAAATATT	270
QY	1256	ATCTATACAGAGCATGACAGGAGACCCTTCAGAGGTATTAATGACGAACATCAGAGT	1315
Db	269	ATCTATACAGAGCATGACAGGAGACCCTTCAGAGGTATTAATGACGAACATCAGAGT	210
QY	1316	AACACATTCCTACAAATCAGCTGGATGCGCCAACTTAAATTTGTAAACATGAGTCAGTGGA	1375
Db	209	AACACATTCCTACAAATCAGCTGGATGCGCCAACTTAAATTTGTAAACATGAGTCAGTGGA	152
QY	1376	CTGTGTGTCTTCGACAGAGTCTCTTCGAGGATATCATCATTTCCGGTTTGTAAATCTTAT	1435
Db	151	CTGTGTGTCTTCGACAGAGTCTCTTCGAGGATATCATCATTTCCGGTTTGTAAATCTTAT	92
QY	1436	TCACCAATATGTTCTATGCTGCTGTAAGGTAAGAACTGTAATATACATCATTTAAATPAC	1495
Db	91	TCACCAATATGTTCTATGCTGCTGTAAGGTAAGAACTGTAATATACATCATTTAAATPAC	32
QY	1496	AAATGTTCTATTATTAACACTT	1515
Db	31	AAAT-TTCATTATTAACACTT	13
RESULT 6			
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LOCUS	AL581997	Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED	
DEFINITION	Homo sapiens cDNA clone CS0DL003YG24 5-PRIME, mRNA sequence.		
ACCESSION	AL581997		
VERSION	AL581997.2	GI:31320228	
KEYWORDS	EST.		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1201)		
TITLE	Li, W.B., Gruber, C., Jesse, J., and Polayes, D.		
JOURNAL	Full-length cDNA libraries and normalization		
COMMENT	On Feb 16, 2001 this sequence version replaced gi:12949550.		
	Contact: Genoscope		
	Genoscope - Centre National de Sequencage		
	BP 191 91006 Evry cedex - France		
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr		
	Library was constructed by life technologies, a division of invitrogen. This sequence belongs to sequence cluster 1287.f For more information about this cluster, see		
	http://www.genoscope.cns.fr/		
	cg1-bin/cluster.cg1seq-CS0DL003BD12QPl6cluster=1287.f. Contact :		
	Feng Liang Email : fliang@lifetech.com URL :		
	http://fulllength.invitrogen.com/ Invitrogen Corporation 1600		
	Faraday Avenue genoscope sequence ID : CS0DL003BD12QPl.		
FEATURES	Location/Qualifiers		
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	/cell_line="RAMOS CELL LINE"		
	/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"		
	/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."		
BASE COUNT	293 a	286 c	277 g
ORIGIN			310 t
			35 others

	Query Match	60.0%:	Score 931.6:	DB 9:	Length 1201:	
	Best Local Similarity	95.5%:	Pred. No. 4.1e-241:			
	Matches 991:	Conservative 10:	Mismatches 29:	Indels 8:	Gaps 4:	
QY	169 TGAATAGAGCATGATGATAGTACCCACAGACAGTCGGGTGTGTAGATTCCCTGATCTGCAA	228				
Db	97 TGTCATCTGGTGATGCCCAAGTCCCACAGACAGTCGGGTGTGTATTTCCCTGATCTGCAA	156				
QY	229 TTCTTCCCGTTCCCTTCATGGAATGTAAGGCTCTCCTTCTCTTGAATGACTTGCATC	288				
Db	157 TTCTTCCCGTTCCCTTCATGGAATGTAAGGCTCTCCTTCTCTTGAATGACTTGCATC	216				
QY	289 CCGTCGTTTTGCTAGAGTTGGGCAANTGTGGATTTCTGGTGGAACCAACCACCAACA	348				
Db	217 CCTCTCGTTTCTAGAGTTGGGCAANTGTGGATTTCTGGTGGAACCAACCACCAACA	276				
QY	349 TACTGTAAATACACTCTTCCAGCAATGACCTACTAGAGTAGATGAGAGTGTCT	408				
Db	277 TACTGTAAATACACTCTTCCAGCAATGACCTACTAGAGTAGATGAGAGTGTCT	336				
QY	409 GCAAAAGAAGGACAGCTCATTTCTCTCTACCATCCGCTATFTTCCGACCCATGAAGC	468				
Db	337 GCAAAAGAAGGACAGCTCATTTCTCTCTACCATCCGCTATFTTCCGACCCATGAAGC	396				
QY	469 CATTAACCTGGAAACATGGAAGGAGCGGCTGTATCCGGGCTCGGGGAACAGAGTGG	528				
Db	397 CATTAACCTGGAAACATGGAAGGAGCGGCTGTATCCGGGCTCTGGAGAACAGAGTGG	456				
QY	529 TATCTACTCTTCCATACAGGCTATGATGTGTGCGCCCCAGGGCGTCAACAATGTTGGC	588				
Db	457 TATCTACTCTTCCATACAGGCTATGATGTGTGCGCCCCAGGGCGTCAACAATGTTGGC	516				
QY	589 TAAAGGCTTGGAGCTGTACTCTCAGGCCCATATCATCTTCCAAAGTCCCAACTACCC	648				
Db	517 TAAAGGCTTGGAGCTGTACTCTCAGGCCCATATCATCTTCCAAAGTCCCAACTACCC	576				
QY	649 TACAGAGGGAACCAACGAGTAGAATTCAGATTAATCACACCCAAGACCTGGACAAAGT	708				
Db	577 TACAGAGGGAACCAACGAGTAGAATTCAGATTAATCACACCCAAGACCTGGACAAAGT	636				
QY	709 CATGTCTGCAGTGAAGGAATTTGACGGGTTCTGTCACTCTTTTCTGCTAGAGACTGG	768				
Db	637 CATGTCTGCAGTGAAGGAATTTGACGGGTTCTGTCACTCTTTTCTGCTAGAGACTGG	696				
QY	769 TAATGAGGAACAAACAGGATTAATCTGAATTTGACTCAGAAGGCTTTGATGACAGTGT	828				
Db	697 TAATGAGGAACAAACAGGATTAATCTGAATTTGACTCAGAAGGCTTTGATGACAGTGT	756				
QY	829 AGATTTTCTTCCCGGAAACAACACTTATCAGAAAGCGGAATTTCTGTACTGTGAGAA	888				
Db	757 AGATTTTCTTCCCGGAAACAACACTTATCAGAAAGCGGAATTTCTGTACTGTGAGAA	816				
QY	889 GCCTTTGGCTTACATACTGGAAATGGGACGGTATTGACACTGGATGATGTCTCCCT	948				
Db	817 GCCTTTGGCTTACATACTGGAAATGGGACGGTATTGACACTGGATGATGTCTCCCT	876				
QY	949 GGCAACCATGATGATGATGATAAAGACACCTAAAACATATCTCATATTGCTTAGCCCT	1008				
Db	877 GGCAACCATGATGATGATGATAAAGACACCTAAAACATATCTCATATTGCTTAGCCCT	936				
QY	1009 T-T-GGGGTGGGAGAACCTTAGAGTCTCAAGTCAAAAGTCGTGGCCCTGTGTCTGTCTG	1067				
Db	937 TGGGGTGGGAGAACCTTAGAGTCTCAAGTCAAAAGTCGTGGCCCTGTGTCTGTCTG	996				
QY	1068 GGACACACGTTCTGACAGGCTGTAGAGGTGACCTTACCTACAGAGGTGAGATGTCATC	1127				
Db	997 GGACACACGTTCTGACAGGCTGTAGAGGTGACCTTACCT-MMAGGTGAGATG-CCATC	1054				
QY	1128 ATGATACTTTGGATGCTGCTCCCAAGAAATTAATGTCAATCTGTGAMACACCAACA	1187				
Db	1055 ATGATACTTTGGATGCTGCTCCCAAGAAATTAATGTGTM-C-----CTGTGTAMMAACAACA	1109				
QY	1188 CTGAACGAGGCTTTCTTT 1205					

Db 1110 CTGACGAGSTTTTCT 1127

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RESULT 7  
BX446370 1201 bp mRNA linear EST 22-MAY-2003  
LOCUS BX446370 Homo sapiens PLACENTA Homo sapiens CDNA clone CLOBA0042B11  
DEFINITION 5-PRIME, mRNA sequence.  
ACCESSION BX446370  
VERSION BX446370.1 GI:31023721  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1201)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 1287.f for  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CLOBA0042B11R1&cluster=1287.f. Contact :  
Peng Liang Email: liliang@life.techn.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID: CLOBA0042B11R1.  
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
with a NotI-Q1igo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 5 vector.  
Library was not normalized."  
BASE COUNT 349 a 256 c 266 g 296 t 34 others  
ORIGIN

Query Match 60.08; Score 931.6; DB 13; Length 1201;  
Best Local Similarity 98.78; Pred. No. 4.1e-241;  
Matches 965; Conservative 5; Mismatches 4; Indels 4; Gaps 3;

QY 386 GAGGAAGTAGGAGGAGGCTGCGCAAAAGCAGACACCTCATCTCTCTTACCACCG 445  
DB |||||||  
QY 67 GATGAAGTAGGAGGAGGCTGCGCAAAAGCAGACACCTCATCTCTCTTACCACCG 126  
DB |||||||  
QY 446 CTAATCTCCGACCCATGAAGCGCATTAACCTGAACACATGGAAGAGCGCTGATATC 505  
DB |||||||  
QY 127 CTAATCTCCGACCCATGAAGCGCATTAACCTGAACACATGGAAGAGCGCTGATATC 186  
DB |||||||  
QY 506 CGGCGCTTGAGAAACAGAGTCGATATCTCTCTTAATACAGCTATGAGTGGCGCC 565  
DB |||||||  
QY 187 CGGCGCTTGAGAAACAGAGTCGATATCTCTCTTAATACAGCTATGAGTGGCGCC 246  
DB |||||||  
QY 566 CAGGCGCTCAACAACTGTTGGCTAAAGGCTTGAGCTGTACTCCAGGCCCATCAT 625  
DB |||||||  
QY 247 CAGGCGCTCAACAACTGTTGGCTAAAGGCTTGAGCTGTACTCCAGGCCCATCAT 306  
DB |||||||  
QY 626 CTTTCCAAAGCTCCCACTACCTACAGAGGAAACACCGAGTAGAATTAACGTTAAC 685  
DB |||||||  
QY 307 CTTTCCAAAGCTCCCACTACCTACAGAGGAAACACCGAGTAGAATTAACGTTAAC 366  
DB |||||||  
QY 686 TACACCCAAAGCTGAGCAAAAGTCATCTGCACTGAAGAATTAACGCTTCTGTC 745

Db 367 TACACCCAAAGCTGAGCAAAAGTCATGCTCAGAGGAAGAATTAACGCTTCTGTC 426  
QY 746 ACTTCTTTTCTGCTAGAGCTGTAATGAGAAACACCGATTAATCTAATTTGACT 805  
DB |||||||  
QY 427 ACTTCTTTTCTGCTAGAGCTGTAATGAGAAACACCGATTAATCTAATTTGACT 486  
DB |||||||  
QY 806 CAGAAGGCTTGTAGCAGAGTGTGATTTTCTTCCCGGAAACAACTTATCAGAA 865  
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QY 866 ACGGAATTTGCTACTGAGAGACCTTTGCTTCTACATCTGAAATGGAAGCTTATGC 925  
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QY 926 ACATGATGATATCTGCTCCCTGCAACCACTGATGCAATTAATAAACACCTTAAA 985  
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QY 607 ACATGATGATATCTGCTCCCTGCAACCACTGATGCAATTAATAAACACCTTAAA 666  
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QY 986 CTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAACCTTAGAGTCAAGTCAAGAGTC 1045  
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QY 1106 CTCACAGGTGAGAGTCCCATCATGATATCTTGGATGCTGCTTCCCAAGAAATATGTC 1165  
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QY 787 CTCACAGGTGAGAGTCCCATCATGATATCTTGGATGCTGCTTCCCAAGAAATATGTC 846  
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QY 1166 ATCCCTGTGTAACACAGCACTGAAAGAGGCTTCTTCTGCACTTGAATATGCTG 1225  
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QY 847 ATCCCTGTGTAACACAGCACTGAAAGAGGCTTCTTCTGCACTTGAATATGCTG 906  
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QY 1226 GATTCCTACCTGGAATATGATATATATTC- TATCAGAGCTGACAGGACCTCT 1284  
DB |||||||  
QY 907 GATTCCTACCTGGAATATGATATATATTCCTTATCAGAGCTGAAAGGACCTCT 966  
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QY 1285 TCAGGTGATATATGCGAAGCAATCAGATACATCTTACAAATCAGCTGATGCC 1344  
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QY 967 TCAGGTGATATATGCGAAGCAATCAGATACATCTTACAAATCAGCTGATGCC 1023  
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QY 1345 CAACCTAAATTTGTACA 1362  
DB |||||||  
QY 1024 CMACTTAATTTGTAAAA 1041

RESULT 8  
BX377118/c 1201 bp mRNA linear EST 08-MAY-2003  
LOCUS BX377118 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
DEFINITION clone CSOD1002YH20 3-PRIME, mRNA sequence.  
ACCESSION BX377118  
VERSION BX377118.1 GI:30448573  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1201)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 1287.f for  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CSOD1002YH20&cluster=1287.f. Contact :



Feng Liang Email : filiang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0D1002B610NP1.  
Location/Qualifiers  
1. 1201

FEATURES  
source

/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="CS0D1002YM20"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."  
BASE COUNT 319 a 250 c 257 g 325 t 50 others  
ORIGIN

Query Match 59.5%; Score 924.6; DB 13; Length 1201;  
Best Local Similarity 93.8%; Pred. No. 3.2e-239;  
Matches 1037; Conservative 15; Mismatches 42; Indels 11; Gaps 9;

430 TCTCTCCATCCATCCGCTATCTCCGACCATGAAAGGCTATACCTGGAAACATGAA 489  
1097 TCATTCTCTCCATCCGCTATCTCCGACCATGAAAGGCTATACCTGGAAACATGAA 1042  
430 GGAGGCGCTGTGATCCGGGCTCTGTGAGAAAGAGTGGGT-ATCTACTCTCCATACAG 548  
1041 AGGAGCGCTGTGATCCGGGCTCTGTGAGAAAGAGTGGGTATCTACTCTCCATACAG 982  
549 CCTATGATGCTGCGGCCAGGGCGTCAACACTGTTGGCTAAAGGGCTTGAAGCTTTGA 608  
981 CCTATGATGCTGCGGCCAGGGCGTCAACACTGTTGGCTAAAGGGCTTGAAGCTTTGA 922  
609 CCTCAGGCGCTATCTCCGACCATGAAAGGCTATACCTGGAAACATGAAAGGCTATAC 668  
921 CCTCAGGCGCTATCTCCGACCATGAAAGGCTATACCTGGAAACATGAAAGGCTATAC 862  
669 TAGAATTCAGCTTAACTACACCC-AAGACTGAGCAAGTATGTCAGTGAAGA 727  
861 TAGAATTCAGCTTAACTACACCCAAAGACTGAGCAAGTATGTCAGTGAAGA 802  
728 ATTGACGGTGTCTGCTACTCTTTTCTGTAGACTGTGTAAGAGAAACACACGG 787  
801 ATTGACGGTGTCTGCTACTCTTTTCTGTAGACTGTGTAAGAGAAACACACGG 742  
788 ATTATTCGATTTGATCTAGAAAGGCTTGTATGATGATTTCTTTCCCGGAGC 847  
741 ATTATTCGATTTGATCTAGAAAGGCTTGTATGATGATTTCTTTCCCGGAGC 682  
848 AAAACACTTTATCAGAAAGGAAATTCGTACTGAGAAAGCTTTGCTTCTACTACT 907  
681 AAAACACTTTATCAGAAAGGAAATTCGTACTGAGAAAGCTTTGCTTCTACTACT 622  
908 GGAATGGGAGCGTTATGACACTGATGATGATGATGATGATGATGATGATGATGATGAT 967  
621 GGAATGGGAGCGTTATGACACTGATGATGATGATGATGATGATGATGATGATGATGAT 562  
968 AAAAAAGACACTTAAATATCTCATATTCCTTACCTTGGGGTGGGAGAACTTA 1027  
561 AAAAAAGACACTTAAATATCTCATATTCCTTACCTTGGGGTGGGAGAACTTA 502  
1028 GAGTCTCAAGTCAAAAGCGTGGCGCTGTGCTGTGCTGTGAGAGCAGCGTTCTGAGG 1087  
501 GAGTCTCAAGTCAAAAGCGTGGCGCTGTGCTGTGCTGTGAGAGCAGCGTTCTGAGG 442  
1088 GTTGGGCTGACCTTACTCTACAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1147  
441 GTTGGGCTGACCTTACTCTACAGTGTGATGATGATGATGATGATGATGATGATGATGAT 382  
1148 TCCCAAGGAAATTAATGTCATCTCTGTGAAACAGCAACACTGAAAGGCTTTCTTTCT 1207  
381 TCCCAAGGAAATTAATGTCATCTCTGTGAAACAGCAACACTGAAAGGCTTTCTTTCT 322

QY 1208 GACCTTCGAGATATGCTGATTTCTCATTGGAGAAATGAATTAATTAATCTTATCAGAG 1267  
DB 321 GACCTTCGAGATATGCTGATTTCTCATTGGAGAAATGAATTAATTAATCTTATCAGAG 262  
QY 1268 ACTGACAGGAGCCCTTTCA-GGTGATATATGCGAAGAAACATCAGATTAATCTCT 1326  
DB 261 ACTGACAGGAGCCCTTTCAAGGATATATGCGAAGAAACATCAGATTAATCTCT 203  
QY 1327 ACAATCAGTGGATGCCCACTTAATTTGTAATGATGATGATGATGATGATGATGATGAT 1386  
DB 202 ACAATCAGTGGATGCCCACTTAATTTGTAATGATGATGATGATGATGATGATGATGAT 144  
QY 1387 CCAGAGAGTGTCTTCAGAGGATATCATTTCCGTTTGTATCTTAATTCACCAATGT 1446  
DB 143 CCAGAGAGTGTCTTCAGAGGATATCATTTCCGTTTGTATCTTAATTCACCAATGT 84  
QY 1447 TCTATGCTGCTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1506  
DB 83 TCTATGCTGCTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 25  
QY 1507 ATTAATCTGAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1531  
DB 24 ATTAATCTGAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1

RESULT 9

LOCUS BX393871 930 bp mRNA linear EST 13-MAY-2003  
DEFINITION BX393871 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens  
cDNA clone CS0DC005YM21 5-PRIME, mRNA sequence.  
ACCESSION BX393871  
VERSION BX393871.1 GI:30624084  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 1287.f for  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DC005AG110P1&cluster=1287.f. Contact :  
Feng Liang Email : filiang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DC005AG110P1.  
Location/Qualifiers  
1. 930

FEATURES  
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/clone="CS0DC005YM21"  
/tissue\_type="NEUROBLASTOMA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 248 a 231 c 214 g 237 t  
ORIGIN

Query Match 55.4%; Score 861; DB 13; Length 930;  
Best Local Similarity 97.8%; Pred. No. 5.1e-222;  
Matches 873; Conservative 0; Mismatches 20; Indels 0; Gaps 0;



OY	153	AGGCGTGAAGTGGACACTGGAATATGAGGCATAGATAGTCCACAGACAGTCCGGTTTATG	212
Db	38	AGGCTGTACCGGTCGGGAATTTCCCGGAGTGGACTGTCTCCACACAGATCGGTTTATG	97
OY	213	ATTCCCTGATCTGGAATTTCTCCCGTTCCTTCATGAGATTTGAAGGCTCTCTTCTTCCT	272
Db	98	ATTCCCTGATCTGCAATTTCTCCCGTTCCTTCATGAGATTTGAAGGCTCTCTTCTTCCT	157
OY	273	TGAATGACTTTCATCCCTCTCTGTTTGTCTGAGAGTTGGAGACATGTTGGATTACTGTGTG	332
Db	158	TGAATGACTTTCATCCCTCTCTGTTTGTCTGAGAGTTGGAGACATGTTGGATTACTGTGTG	217
OY	333	AACCAAGCCCAACCACTACTCTAATATCACTCTTCTGACCAATGACTGACTAGAGAG	392
Db	218	AACCAAGCCCAACCACTACTCTAATATCACTCTTCTGACCAATGACTGACTAGAGAG	277
OY	393	TGATGAGAGAGTCTCTGCAAAAGAAGGAGACCTCATCTCTCTACCATCGGCTTACT	452
Db	278	TGATGAGAGAGTCTCTGCAAAAGAAGGAGACCTCATCTCTCTACCATCGGCTTACT	337
OY	453	TCCGACCCCATGAGCGCATTAACCTTGGAACACATGGAAGAGACGCTTGATGTCGGGCTC	512
Db	338	TCCGACCCCATGAGCGCATTAACCTTGGAACACATGGAAGAGACGCTTGATGTCGGGCTC	397
OY	513	TGGAGAACAGAGTGGTATCTTACCTCTCTCTATACAGCTATAGATGTGCGGCCACAGGCG	572
Db	398	TGGAGAACAGAGTGGTATCTTACCTCTCTCTATACAGCTATAGATGTGCGGCCACAGGCG	457
OY	573	TCAACAACCTGGTGGCTTAAAGGGCTTGGAGCTTTTACTCTCCAGGCCCATCATCTTCCA	632
Db	458	TCAACAACCTGGTGGCTTAAAGGGCTTGGAGCTTTTACTCTCCAGGCCCATCATCTTCCA	517
OY	633	AAGCTCCCACTACCTTACAGAGGAAACACCCGATGATGAATTCAGTAACTTACACACC	692
Db	518	AAGCTCCCACTACCTTACAGAGGAAACACCCGATGATGAATTCAGTAACTTACACACC	577
OY	693	AAGACCTGGACAAGTCACTGTCTGACAGGAAGAAATTGAGGGTTCCTCTCACTCTT	752
Db	578	AAGACCTGGACAAGTCACTGTCTGACAGGAAGAAATTGAGGGTTCCTCTCACTCTT	637
OY	753	TTTCTGCTAGAGACTGTATATGAGAAACAACACGGATTAATCTGAATTTGACTCAGAAG	812
Db	638	TTTCTGCTAGAGACTGTATATGAGAAACAACACGGATTAATCTGAATTTGACTCAGAAG	697
OY	813	CTTTGATGACAGTGGTAGATTTTCTTCCCGGAACAACAATTATCAGAAGACGGAA	872
Db	698	CTTTGATGACAGTGGTAGATTTTCTTCCCGGAACAACAATTATCAGAAGACGGAA	757
OY	873	TTTCTGCTACGTGAGAAAGCTTTGCTTCTACACTCTGAAATGGAGCGTTATGACACACGG	932
Db	758	TTTCTGCTACGTGAGAAAGCTTTGCTTCTACACTCTGAAATGGAGCGTTATGACACACGG	817
OY	933	ATGATATCTGTCTCCCTGGCAACCATATGATTCGAATTAATAAAGACACTTAATATCTC	992
Db	818	ATGATATCTGTCTCCCTGGCAACCATATGATTCGAATTAATAAAGACACTTAATATCTC	877
OY	993	ATATTGCGTTAGCCCTTGGGGTGGGAGAACCTTAGAGTCTCAAGTCAAAAGTC	1045
Db	878	ATATTGCGTTAGCCCTTGGGGTGGGAGAACCTTAGAGTCTCAAGTCAAAAGTC	930
RESULT 10			
BX386928			
LOCUS	BX386928	1006 bp	linear
DEFINITION	BX386928	Homo sapiens NEUROBLASTOMA COR 25-NORMALIZED Homo sapiens	EST 08-MAY-2003
ACCESSION	BX386928	CDNA clone CS0DC003B10 5'-PRIME, mRNA sequence.	
VERSION	BX386928.1	GI:30447485	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		

REFERENCE	1 (bases 1 to 1006)					
AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.					
TITLE	Full-length cDNA libraries and normalization					
JOURNAL	Unpublished					
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1287.f For more information about this cluster, see <a href="http://www.genoscope.cns.fr/cgl-bin/cluster.cgi?seq-CSIDC001ZF080Plc&amp;cluster=1287.f">http://www.genoscope.cns.fr/ cgl-bin/cluster.cgi?seq-CSIDC001ZF080Plc&amp;cluster=1287.f</a> . Contact : Feng Liang Email : <a href="mailto:liang@life.com">liang@life.com</a> / <a href="mailto:invitro@corp.lifetech.com">invitro@corp.lifetech.com</a> URL : <a href="http://fulllength.invitrogen.com/">http://fulllength.invitrogen.com/</a> , Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSIDC001ZF080Pl.					
FEATURES						
source	Location/Qualifiers 1..1006 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSIDC003YB10" /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED" /clone_id="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized." BASE COUNT      252 a    236 c    258 g    245 t       15 others ORIGIN					
Query Match	55.4% ; Score 860 ; DB 13 ; Length 1006 ;					
Best Local Similarity	97.9% ; Pred. No. 9,8e-22 ;					
Matches	868 ; Conservative 11 ; Mismatches 7 ; Indels 1 ; Gaps 1 ;					
Dn	1 GTGATTGGTAATCTTGTCGTGCAGACAGACAGAAAGAGGATGGGTCAGAAAACATGC 60					
Dn	119 GTGATTGKATCTTGTCGTGCAGACAGACAGAAAGAGGATGGGTCAGAAAACATGC 178					
Dn	61 CCTGCCGACACAGACAGACAGGCACTAGTTGGACAGGGGTCCTGACTCAGACTTAACATCG 120					
Dn	179 CCTGCCGACACAGACAGACAGGCACTAGTTGGACAGGGGTCCTGACTCAGACTTAACATCG 238					
Dn	121 CTGTGTCTCGTGCTTTTCTACTGTCTCTGAAAAAGCCCTGAAGTGCGACTGAATATGAGCA 180					
Dn	239 CTGTGTCTCGTGCTTTTCTACTGTCTCTGAAAAAGCCCTGAAGTGCGACTGAATATGAGCA 298					
Dn	181 TAGATGATGCCCCACAGACAGTCGGTTGTGATTCCTGATCTGCATTTCTCCGGTTC 240					
Dn	239 TAGATGATGCCCCACAGACAGTCGGTTGTGATTCCTGATCTGCATTTCTCCGGTTC 358					
Dn	241 CTTCATGTGATTTGAAGGCTCTCCTTTCTCTTCTTGAATGACTTTGGATCCCTCTCGTTTC 300					
Dn	359 CTTCATGTGATTTGAAGGCTCTCCTTTCTCTTCTTGAATGACTTTGGATCCCTCTCGTTTC 418					
Dn	301 TGAGAGTTGGACAATGTTGGATTACTGCTGAGAACCAAGCCACCACATACTGTAAATAC 360					
Dn	419 TGAGAGTTGGACAATGTTGGATTACTGCTGAGAACCAAGCCACCACATACTGTAAATAC 478					
Dn	361 ACTCTTCTGACCAATGACCTGACAGAGAATGATGAGAGAGTGCTGCAAAAAGAACGC 420					
Dn	479 ACTCTTCTGACCAATGACCTGACAGAGAATGATGAGAGAGTGCTGCAAAAAGAACGC 538					
Dn	421 AGACTCATTTCTCTCTACATCCGCTATCTTTCCGACCAATGAAGCGATTAACCTGGA 480					
Dn	539 AGACTCATTTCTCTCTACATCCGCTATCTTTCCGACCAATGAAGCGATTAACCTGGA 598					
Dn	481 CACATGGAAGAGCGCTGTGTATCCGGGCTCTTGAGAACAAGAGTCGGATATCTACTCTCC 540					
Dn	599 CACATGGAAGAGCGCTGTGTATCCGGGCTCTTGAGAACAAGAGTCGGATATCTACTCTCC 658					
Dn	541 TCATACAGCTATGATGCTCGCCCCCAGGGGCTCAACAACATGCTGCTAAAGGCTTGG 600					

Db 659 TCATACAGCCTATGATGCTGCGCCCGGCGTCAACAAGTGGTGAAGGGCTTG 718  
QY 601 ACCTGTACCTCCAGGCCATACATCTTCGAAGCTCCCACTACCTACAGAGGAAA 660  
Db 719 AGCTGTACCTCCAGGCCATACATCTTCGAAGCTCCCACTACCTACAGAGGAAA 778  
QY 661 CCACGAGTGAATTCACAGCTTACACACCCAGACCTGACCAAAAGTCTGTCAGT 720  
Db 779 CCACGAGTGAATTCACAGCTTACACACCCAGACCTGACCAAAAGTCTGTCAGT 838  
QY 721 GAAAGGATTCAGAGGCTTCTGCTACTCTTTCTTCTGCTAGACCTGTAATGAGAGAA 780  
Db 839 KAAAGGAATTCAGAGGCTTCTGCTACTCTTTCTTCTGCTAGACCTGTAATGAGAGAA 898  
QY 781 AACACGATTCATGTAATTCATGCTAGCAGAGGCTTGTATGATGATTTCTTTC 840  
Db 899 AACACGATTCATGTAATTCATGCTAGCAGAGGCTTGTATGATGATTTCTTTC 958  
QY 841 CCGGACCAACCAACTTATCAGAGAGCAAAATTCCTGCTAGAGAG 887  
Db 959 CCGGACCAACCAACTTATCAGAGAGCAAAATTCCTGCTAGAGAG 1004

RESULT 11  
BX385101/c 984 bp mRNA linear EST 08-MAY-2003  
DEFINITION BX385101 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED  
ACCESSION Homo sapiens cDNA clone CS0DL006YD12 3-PRIME, mRNA sequence.  
VERSION BX385101  
KEYWORDS BX385101.1 GI:30453308  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 984)  
AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 1287.f for  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DL006YD12&cluster=1287.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DL006YD12B05NP1.  
Location/Qualifiers

FEATURES  
source  
1. 984

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/db\_xref="taxon:9606"  
/clone="CS0DL006YD12"  
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/cell\_line="RAMOS CELL LINE"  
/clone\_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT  
25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."  
BASE COUNT 269 a 205 c 213 g 277 t 20 others

Query Match 55.1%; Score 855.6; DB 13; Length 984;  
Best Local Similarity 95.0%; Pred. No. 1.5e-220;  
Matches 927; Conservative 8; Mismatches 34; Indels 7; Gaps 5;

QY 555 ATGCTGCGCCCGGCGCTCAACACTGTTGGCTAAAGGGCTTGAGACTTGACTCCA 614

Db 970 WTGATSTGCCCCCGGCGCTCAACACTGTTGGCGMAAAG--ATTGAGCTTKACCTCCA 914  
QY 615 GGGCCATATCTCTTCCAAAGCTCCCACTACCTACAGAGGAAACACGAGTAGAT 674  
Db 913 GGGCCATATAT-CTTCCAAAGCTCCCACTACCTACAGAGGAAACACGAGTAGAT 855  
QY 675 TCACGTTAATACACCCAGACCTGAGCAAAATGCTCTCAGTGAAGAAATGAGC 734  
Db 854 TCACGTTAATACACCCAGACCTGAGCAAAATGCTCTCAGTGAAGAAATGAGC 795  
QY 735 GTGTTCTGCTCACTTCTTTCTGCTAGAGCTGTAATGAGAAACAACGAGATTATC 794  
Db 794 GTGTTCTGCTCACTTCTTTCTGCTAGAGCTGTAATGAGAAACAACGAGATTATC 735  
QY 795 TGAATGTACTAGAAAGCTTGTATGACAGTGTGATTTG-TTTTCCGGAACAACA 853  
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QY 854 CTTTATCAGAAAGCAAAATTCCTGCTAGAGAGCCCTTCTCTACATCTGGAATG 913  
Db 674 CTTTATCAGAAAGCAAAATTCCTGCTAGAGAGCCCTTCTCTACATCTGGAATG 615  
QY 914 GGAAGTTATGCACTGATGATGTCTCTCCCTGCGCAACATGATGATGAATAAA 973  
Db 614 GGAAGTTATGCACTGATGATGTCTCTCCCTGCGCAACATGATGATGAATAAA 555  
QY 974 AGACACCTAAACTATCATATTCCTAGAGCTTGGGCTGGGAGAACCTTAGAGTC 1033  
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QY 1034 CAAGTCAAAAGTGTGGCCCTGCTGCTGCTGCTGAGAGAGGCTTCTGAGGCTTGA 1093  
Db 494 CAAGTCAAAAGTGTGGCCCTGCTGCTGCTGCTGAGAGAGGCTTCTGAGGCTTGA 435  
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Db 434 GCTGACCTTACCTCAGAGTGAATGTCCCATCATGATCTTGGATGCTGCTCCAA 375  
QY 1154 GGAATTAATGTCTCTCTGCTGAGACAGCAACACTGAGAGAGCTTCTTCTGACCTT 1213  
Db 374 GGAATTAATGTCTCTCTGCTGAGACAGCAACACTGAGAGAGCTTCTTCTGACCTT 315  
QY 1214 CGAGATATCTGATTCCTCAGTGAATTAATTAATTCCTATCAGAGTAC 1273  
Db 314 CGAGATATCTGATTCCTCAGTGAATTAATTAATTCCTATCAGAGTAC 255  
QY 1274 AGGAGACCTCTCAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1333  
Db 254 AGGAGACCTCTCAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 196  
QY 1334 AGCTGATGCCCACTTAATTTGTAACATGATGAGTGGAGCTGTGCTCCAGAGA 1393  
Db 195 AGCTGATG-CCAACTTAATTTGTAACATGATGAGTGGAGCTGTGCTCCAGAGA 137  
QY 1394 GTGTCTTCGAGGATCATCATTTCCGCTTTGTAATCTTATTCACCAATGTTCTATG 1453  
Db 136 GTGTCTTCGAGGATCATCATTTCCGCTTTGTAATCTTATTCACCAATGTTCTATG 77  
QY 1454 CTGCTAGGTAACCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1513  
Db 76 CTGCTAGGTAACCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATCT 17  
QY 1514 CTAGAAAGTTGAAT 1529  
Db 16 AGDNNKKATGMAAT 1

RESULT 12  
AK011670 1376 bp mRNA linear HTC 05-DEC-2002  
DEFINITION AK011670 Mus musculus 10 days embryo whole body cDNA, RIKEN full-length  
enriched library, clone:2610034I10 product:Nrg1 Interacting factor

ACCESSION	3-1like1 (S. pombe), full insert sequence
VERSION	AK011670
KEYWORDS	AK011670.1 GI:12847943
SOURCE	HTC; CAP trapper.
ORGANISM	Mus musculus (house mouse)
	Mus musculus

REFERENCE	1
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
PMID	99279253
DOI	10349636
REFERENCE	2

QY	307	TTGGGACAAATTGGTGGATTACTGCGTGGGAACCAAGCCACACATACTGTAAATPACCTTT	366
Db	188	CTGGGACAAATTTGGGATTACTGCTGTGTGGACCACCAAGCCACCCATCTACTGTAAATPACCTTT	247
QY	367	CCTGACCAATGACCTGACTGAGGAAGTGAATGGAGAGGTGCTGCMAAAGGAAGGACGACCT	426
Db	248	CCTGACCAATGACCTGAGCGAGGAGGTGATGAGAGAGGCTCTGCMAAAGGAAGGACGACCTT	307
QY	427	CATTCTCTCCACCATCCGCTTAICTTTCGCCACCATGAAGGCGATTAACCTTGGACACATG	486
Db	308	CATTCTCTCCACCATCCGCTTAATTTTCGCCACCATGAAGGACATTAACCTTGGAAAACTGT	367
QY	487	GAAGGAGCGCTGGTGTATCCGGGCTCTGGAAACAGAGTGGTATCTACTCTCCCATAC	546
Db	368	GAAGGAGTGTGTGTGATCCGGGCTCTGGAAACAGAGTCCGCTGTACTCTCCCATAC	427
QY	547	AGCCTATGATGCTGTGGGCCCAAGGGCGTCACAACTGTGTGGCTAAAGGGCTGGAGCTTG	606
Db	428	AGCCTATGATGCTGGGACCCCAAGGAGTCCAAAGCTGTGTGGCCCAAGGGCGCTGGAACTTG	487
QY	607	TACCTCCAGGGCCCACTACCTCTCCAAAGTCCCAACATACCTCTACAGGGGAAACCAACCG	666
Db	488	CACATACCAAGGCCCATCCACCTCTCCAGAGCTCCAGACTACCCCAAGAGGGAGCTCACCG	547
QY	667	AGTAGAATTCACGCTTAATCTACACCCCAAGACCTGGACCAAAAGTCACTGTGCAAGTAAAG	726
Db	548	ACTAGAATTCAGTGTGAACCCGACGCAAGACCTGGACCAAAAGTCACTGTACACTGAGAG	607
QY	727	AATTGAGCGGTCTTCTGTCACTTCTTTTCTGTGTGAGACTGTGAATGAGAACCAACACG	786
Db	608	GGTTGGGAAGTCTCTGTCACTTCTTTTCTGTGTGAGAGGTGAATGAGAACCAACCCG	667
QY	787	GATTAAATCTGAATGTACTCAGAAGGCTTGTATGCAAGGTGGTAAGATTTCTTCCCGGAA	846
Db	668	GATCAGCTGGAATGTACTCAGAAGACTTTTATGCAAGTGCACGCTTCTTTTCCCAAGA	727
QY	847	CAAAACAATTATCAGAAGACGAAATTTCTGTCACTGGAGAAACCTTTGCTTCTACATAC	906
Db	728	CAGCAACTTATCAGAAATTTGAAATCTTTCATTTGAAAAAGCCTTTGCTTTCATAC	787
QY	907	TGGAATGGGAGGTTATGCACACGAGGATGATGATGCTGTCCTCGCAACCATGATGATCG	966
Db	788	TGGAATGGGAGGTTGTGCACACTGGAATGAATGTCTCTCCCTGGCAATATGATGAGCG	847
QY	967	AATAAAAAGACACTTAAATTAATCTATCTCATATTTGCTTACCTCTGGGGTGGGAGAACCTT	1026
Db	848	AATCAAAAACACCTTAAAGTGTGGCATCTTCGCTTACTCTTGGAGTGGGGAACAATT	907
QY	1027	AGAGTCTCAATCAAAAGTCGTGGCCCTGTGTGTGTGTCTGTGGAGACAGCTTCTGACGG	1086
Db	908	AGAGTCTCCAAATCAAAAGTTGTGGCCCTGTGTGTGTGTCTGTGGGGCACTGTCTCAAGG	967
QY	1087	TGTTGAGGCTACCTTCTACTCACAAGGTGAGATGTGCCATATGATGATTTTGGATGACGC	1146
Db	968	AGTGGAGGCGCACTTTACTCTCACAAGTGAATGTGCCACATGATGTCTTGGAGTGTGC	1027
QY	1147	TTTCCCAAGGAATTAATGTCACTCTGTGGAACACAGCAAACTGAACGAGGCTTCTCTTC	1206
Db	1028	TTTCCAAAGGATCAATGTCACTCTTGTGGAACACAGCAAACTGAAAGAGGCTTCTTTC	1087
QY	1207	TGACCTTCGAGATATGCTGGATTTCTCACTTGGAGAAATTAAGATTAATTAATTCATACGA	1266
Db	1088	TGACCTTCGAAATAATGCTGGGTCTTCACTTGGAGAAATTAAGATTAATTAATTCATACGTA	1147
QY	1267	GACGACACGGGACCCCTCTCAGTGGGTATTAATTCAGAAATAATCAGATAC	1318
Db	1148	GACGACACGGGACCCCTCTCGTGGGTTTAATGCAAGGACGTCAAGGACAC	1199

DEFINITION	AGENCOURT 10422791 NIH_MGC_109 Homo sapiens cDNA clone IMAGE:6650148 5', mRNA sequence.
ACCESSION	U0859307
VERSION	U0859307.1
KEYWORDS	EST.
ORGANISM	Homo sapiens (human)
SOURCE	Homo sapiens
REFERENCE	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE	1 (bases 1 to 929)
AUTHORS	NIH-MGC <a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a> .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.lnl.gov">http://image.lnl.gov</a> Plate: LCM2894 row: 0 column: 12 High quality sequence stop: 754.
FEATURES	Location/Qualifiers
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	/db_xref="taxon:9606"
	/clone="IMAGE:6650148"
	/tissue_type="teratocarcinoma, cell line"
	/lab_host="DH10B (phage-resistant)"
	/clone_lib="NIH_MGC_109"
	/note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCCGAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT	251 a 212 c 218 g 247 t 1 others
ORIGIN	
Query Match	54.7%; Score 850.2; DB 13; Length 929;
Best Local Similarity	96.0%; Pred. No. 4.3e-219;
Matches	893; Conservative 0; Mismatches 34; Indels 3; Gaps 2;
QY	491 GAGCGCTGTGATCCGGGCTCTGAGAAACAGTCGGTATCTACTCATACAGCC 550
Db	1 GAGGCGCTGTGATCCGGGCTCTGAGAAACAGTCGGTATCTACTCATACAGCC 60
QY	551 TATGATCTGTGGCCCAAGGGGCTGAACAACGTGGTGAAGGGCTTGAGCTTAC 610
Db	61 TATGATCTGTGGCCCAAGGGGCTGAACAACGTGGTGAAGGGCTTGAGCTTAC 120
QY	611 TCCAGGCCAATACATCTCTTCCAAAGCTCCCACTACCTACAGAGGGAACACAGTA 670
Db	121 TCCAGGCCAATACATCTCTTCCAAAGCTCCCACTACCTACAGAGGGAACACAGTA 180
QY	671 GAATTCACAGTTAACTACACCAAGACCTGAGACAAAGTCATGTGCAAGTAAGAAAT 730
Db	181 GAATTCACAGTTAACTACACCAAGACCTGAGACAAAGTCATGTGCAAGTAAGAAAT 240
QY	731 GAGCGTCTTCTGCACTCTTCTTCTGCTGAGACTGGTATGAGGAACAAACAGATT 790
Db	241 GAGCGTCTTCTGCACTCTTCTTCTGCTGAGACTGGTATGAGGAACAAACAGATT 300
QY	791 AATTCGAATGTACTACAGAGGCTTTATGACAGGTGATGATTTCTTCCGGAAACAA 850
Db	301 AATTCGAATGTACTACAGAGGCTTTATGACAGGTGATGATTTCTTCCGGAAACAA 360
QY	851 CAACCTTATCAGAGACGGAATTTCTGCACTGAGAGAACCTTTTCTTACATACCTGA 910



